Amendments to the Specification:

Please add the paper copy of the Sequence Listing submitted herewith to the specification prior to the Abstract.

Please replace the original title on page 1 with the following amended title:

ANTIBODIES TO ~~ERYTHROPOEITIN~~ **ERYTHROPOIETIN** RECEPTOR AND USES THEREOF

Please replace the paragraph beginning on page 1, line 1 with the following amended paragraph:

This application is a continuation-in-part of U.S. patent application Ser. No. ~~_____~~ **10/821,491**, filed April 9, 2004, the specification of which is incorporated herein by reference.

Please replace the paragraph beginning on page 5, line 22, with the following amended paragraph:

In another aspect, the invention pertains to novel linking sequences. In a preferred embodiment the novel linking sequence connects a first polypeptide sequence and a second polypeptide sequence to form a single polypeptide chain, wherein said first polypeptide sequence is capable of binding a ligand, and said second polypeptide sequence is capable of binding a ligand, and wherein said linking sequence comprises one or more amino acid sequences selected from the group consisting of Gly-Phe-Lys-Asp-Ala-Leu-Lys-Gln-Pro-Met-Pro-Tyr-Ala-Thr-Ser (SEQ ID NO:~~37~~ **27**); Gly-His-Glu-Ala-Ala-Ala-Val-Met-Gln-Val-Gln-Tyr-Pro-Ala-Ser (SEQ ID NO:4); Gly-Pro-Ala-Lys-Glu-Leu-Thr-Pro-Leu-Lys-Glu-Ala-Lys-Val-Ser (SEQ ID NO:3); and Gly-Glu-Asn-Lys-Val-Glu-Tyr-Ala-Pro-Ala-Leu-Met-Ala-Leu-Ser (SEQ ID NO:2).

Please replace the paragraph beginning on page 36, line 13, with the following amended paragraph:

V. Novel Linker Sequences

The invention also provides novel linker sequences for connecting a first polypeptide sequence and a second polypeptide sequence to form a single polypeptide. In a preferred embodiment the novel linking sequence connects a first polypeptide sequence and a second polypeptide sequence to form a single polypeptide chain, wherein said first polypeptide sequence is capable of binding a ligand, and said second polypeptide sequence is capable of binding a ligand, and wherein said linking sequence comprises one or more amino acid sequences selected from the group consisting of Gly-Phe-Lys-Asp-Ala-Leu-Lys-Gln-Pro-Met-Pro-Tyr-Ala-Thr-Ser (SEQ ID NO:~~37~~27); Gly-His-Glu-Ala-Ala-Ala-Val-Met-Gln-Val-Gln-Tyr-Pro-Ala-Ser (SEQ ID NO:2); Gly-Pro-Ala-Lys-Glu-Leu-Thr-Pro-Leu-Lys-Glu-Ala-Lys-Val-Ser (SEQ ID NO:3); and Gly-Glu-Asn-Lys-Val-Glu-Tyr-Ala-Pro-Ala-Leu-Met-Ala-Leu-Ser (SEQ ID NO:4).

Please replace the paragraph beginning on page 37, line 11, with the following amendment paragraph:

Various single stranded oligonucleotides encoding Ab12 scFvs were co-transformed with a linearized "gapped" vector derived from pYD1 (Invitrogen, Carlsbad, CA) into yeast by techniques well known to practitioners in the art. **Functional cell**~~Cell~~ surface protein expression was compared by incubating the transformed yeast with increasing concentrations of soluble EpoR (EposR) at 37°C (FIG. 2). Bound antigen was detected using a monoclonal antibody to EpoR, MAB307 obtained commercially from R and D Systems (Minneapolis, MN) followed by anti-mouse phycoerythrin (PE, Southern Biotech, Birmingham, AL). The Ab12 scFv construct which showed the highest expression used linker 41 (SEQ ID NO:2) as the tether linker and linker 40 (SEQ ID NO:3) as the scFv linker (hereinafter Ab12 41/40). This construct was used in all subsequent FACS experiments as described below.

Please replace the paragraph beginning on page 39, line 7, with the following amended paragraph:

For Round 1 off-rate FACS, each library sample was compared to Ab12 scFv yeast (WT control) for evidence of a population of cells having an increased FL2 fluorescence (and, therefore, a potentially longer off-rate). In each case, the brightest 1% of cells in the FL2 axis were gated, collected, and re-grown in media (Round 1 output). For Round 2 off-rate FACS, the identical cell incubation procedure was performed on each Round 1 library output for some libraries; for others, the Round 2 FACS involved additional reagents to detect surface expression. For each Round 2 off-rate FACS analysis, a gate was drawn around the top 0.1% of cells in the FL2 axis, and this gate was superimposed on all Round 1 library outputs, where applicable. Libraries displaying a population of cells having a higher FL2 than those in the WT gate were selected for FACS, those with no cells ~~outside~~ **inside** of the reference gate were not analyzed further. For those selected libraries, the brightest 0.1% of cells in the FL2 axis were gated and collected. An aliquot was plated on selective media for yeast (SD or "single dropout") for yeast colony isolation and the remainder were grown as liquid cultures for future cell analysis.

Please replace Table 2 beginning on page 43, line 1, with the following amended Table 2:

Table 2

Name	K_{on} (1/M x s)	K_{off} (1/s)	K_d (nM)
Ab12	1.4×10^{5}	1.3×10^{-3}	11
Ab12.6	1.5×10^{5}	4.8×10^{-3}	32
Ab12.56	9.4×10^{54}	1.9×10^{-3}	20
Ab12.17	1.4×10^{5}	4.5×10^{-5}	0.33
Ab12.25	6.5×10^{4}	7×10^{-5}	1
Ab12.61	8.5×10^{4}	9.0×10^{-5}	1
Ab12.70	1.6×10^{5}	9.9×10^{-4}	6
Ab12.76	2.1×10^{5}	9.9×10^{-5}	0.48

Please replace the paragraph beginning on page 50, line 13, with the following amended paragraph:

Example 19: Activity of soluble scFv in a bioassay

The soluble scFvs produced by LT-28-8A and NHS-R1 output scFv clones 33, 34, 38, 40, 41, and 44 were tested in a neutralization bioassay as described in WO 01/58956. All scFv preparations showed IC_{50} values of about $1x10^{-7}$ to $2x10^{-7}$ M. Linker sequence 33 is SEQ ID NO:~~37~~27; Linker sequence 34 is SEQ ID NO:4; Linker sequence 40 is SEQ ID NO:3; Linker sequence 41 is SEQ ID NO:2.